

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2001, 13:35:37 ; Search time 62.8 Seconds
(without alignments)
268.371 Million cell updates/sec

Title: US-09-668-482-2
Perfect score: 2563
Sequence: 1 MGLYTLMTFLCTIVLPVLL.....GPTIYPVDNLPTKTSYVRN 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2563	100.0	492	1	CP26_BRARE
2	1741	67.9	497	1	CP26_HUMAN
3	1734	67.7	497	1	CP26_MOUSE
4	552.5	21.6	472	1	C901_ARATH
5	481	18.8	464	1	CP85_LYCES
6	450	17.6	490	1	C883_ARATH
7	375	14.6	519	1	C881_MAIZE
8	363	14.2	492	1	C136_MYCTU
9	350.5	13.7	518	1	CP3R_ONCMY
10	343.5	13.4	501	1	CP36_RABIT
11	339.5	13.2	490	1	CPC9_HUMAN
12	339.5	13.2	490	1	CPCA_HUMAN
13	333	13.0	503	1	CP39_RAT
14	331	12.9	505	1	C4D8_DROME
15	330.5	12.9	459	1	CPXN_ANASP
16	330.5	12.9	520	1	CP84_ARATH
17	329	12.8	504	1	CP3G_MOUSE
18	328.5	12.8	530	1	CP51_YEAST
19	326	12.7	503	1	CP3T_PIG
20	326	12.7	503	1	CP51_PIG
21	324.5	12.7	503	1	CP33_HUMAN
22	324.5	12.7	507	1	CP3S_BOVIN
23	324	12.6	511	1	CP45_RABIT
24	323.5	12.6	492	1	C131_DROME
25	323.5	12.6	508	1	CP48_RAT
26	322.5	12.6	500	1	CPCB_RAT
27	322.5	12.6	503	1	CP3C_CANFA
28	322.5	12.6	503	1	CP3E_CAVPO
29	320	12.5	502	1	CP34_HUMAN
30	320	12.5	507	1	C4DE_DROME
31	318	12.4	503	1	CP51_HUMAN
32	317.5	12.4	496	1	C7B1_THLAR
33	317	12.4	503	1	CP51_RAT
					P79739 brachydanio
					O43174 homo sapien
					O55127 mus musculu
					Q42569 arabidopsis
					Q43147 lycopersico
					O23051 arabidopsis
					Q43246 zea mays (m
					P95099 mycobacteri
					O42563 oncorhynch
					P11707 oryctolagus
					P11712 homo sapien
					P11713 homo sapien
					P51538 rattus norv
					Q9vs79 drosophila
					P29980 anabaena sp
					Q42600 arabidopsis
					Q64481 mus musculu
					P10614 saccharomyc
					P79401 sus scrofa
					O46420 sus scrofa
					P05184 homo sapien
					P79102 bos taurus
					P14579 oryctolagus
					Q9vrf0 drosophila
					P24464 rattus norv
					P08683 rattus norv
					P24463 canis famil
					Q64417 cavia porce
					P08684 homo sapien
					O46051 drosophila
					Q16850 homo sapien
					P49264 thlaspi arv
					Q64654 rattus norv

34	315.5	12.3	489	1	CP26_CANFA	O62671 canis famil
35	315	12.3	499	1	C719_SOYBN	O81970 glycine max
36	315	12.3	511	1	CP47_RABIT	P14581 oryctolagus
37	314.5	12.3	503	1	CP3F_CAVPO	Q64406 cavia porce
38	314	12.3	504	1	CP32_RAT	P05183 rattus norv
39	314	12.3	510	1	C4DK_DROME	Q9w011 drosophila
40	313.5	12.2	501	1	C4D2_DROME	Q27589 drosophila
41	311.5	12.2	490	1	C7DB_LOTJA	O22307 lotus japon
42	311.5	12.2	490	1	CPCJ_HUMAN	P33261 homo sapien
43	311.5	12.2	502	1	CP35_HUMAN	P20815 homo sapien
44	311.5	12.2	504	1	CP3B_MOUSE	Q64459 mus musculu
45	311	12.1	503	1	CP3O_SHEEP	Q29496 ovis aries

ALIGNMENTS

```
RESULT 1
CP26_BRARE
ID CP26_BRARE STANDARD; PRF; 492 AA.
AC P79739;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094702; PubMed=8939936;
RA White J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Bonasoro J.,
RA Hsu K.E., Dilworth F.J., Jones G., Petkovich M.;
RT "Identification of the retinoic acid-inducible all-trans-retinoic
RT acid 4-hydroxylase."
RL J. Biol. Chem. 271:29922-29927(1996).
CC -!- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEREOISOMER 9-CIS-RA. CAPABLE OF 4-HYDROXYLATION; HYDROXYLATION.
CC RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED FORMS OF RA,
CC INCLUDING 4-OH-RA AND 4-OXO-RA.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RETINOIC ACIDS (RA).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U68234; AAC60045.1; -.
CC ZFIN; ZDB-GENE-990415-44; cyp26.
CC InterPro; IPR001128; -.
CC Pfam; PF00067; P450; 1.
CC PRINTS; PR00385; P450.
CC PROSITE; PS00086; CYTOCHROME_P450; 1.
CC Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum.
FT BINDING 438 438 HEME (BY SIMILARITY).
SQ SEQUENCE 492 AA; 56281 MW; FD471435B2F30509 CRC64;
```

Query Match 100.0%; Score 2563; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 2.9e-140;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGLYTLMTVFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPFGTGLPFIGETLQL 60
Db 1 MGLYTLMTVFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPFGTGLPFIGETLQL 60
QY 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSQWPASVRTIL 120
Db 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSQWPASVRTIL 120
QY 121 GSDTSLNVHGQHKKKKAIMRAFSRDALEHYIPVIOQEVKSAIQEWLQKDSCLVYPPEM 180
Db 121 GSDTSLNVHGQHKKKKAIMRAFSRDALEHYIPVIOQEVKSAIQEWLQKDSCLVYPPEM 180
QY 181 KKLMFRIAMRILLGFEPEQIKTDEQELVEAFEMIKNLFSLPIDVPFSGLYRGLRARNFI 240
Db 181 KKLMFRIAMRILLGFEPEQIKTDEQELVEAFEMIKNLFSLPIDVPFSGLYRGLRARNFI 240
QY 241 HSKTEENIRKKIQDDNENEQYKDALQLLIIENSRSDPEFSLQAMKEAATELLFGGHET 300
Db 241 HSKTEENIRKKIQDDNENEQYKDALQLLIIENSRSDPEFSLQAMKEAATELLFGGHET 300
QY 301 TASTATSLVMFLGLNTEVVQKRVREVEQKVEGMVTPGKGLSMELLQDKLYTGCVIKETL 360
Db 301 TASTATSLVMFLGLNTEVVQKRVREVEQKVEGMVTPGKGLSMELLQDKLYTGCVIKETL 360
QY 361 RINPPVPGGFRVALKTEFELNGYQIPKGNVVIYSICDTHDVADVPFNKEEFQPEREMSKGL 420
Db 361 RINPPVPGGFRVALKTEFELNGYQIPKGNVVIYSICDTHDVADVPFNKEEFQPEREMSKGL 420
QY 421 EDGSRFNYIPFGGGSRMCVKGKEFAKVLKIFLVELTQHNCNWLNSGPTMTKGTIYPVD 480
Db 421 EDGSRFNYIPFGGGSRMCVKGKEFAKVLKIFLVELTQHNCNWLNSGPTMTKGTIYPVD 480
QY 481 NLPTKFTSYVRN 492
Db 481 NLPTKFTSYVRN 492

RESULT 2
CP26_HUMAN
ID CP26_HUMAN STANDARD; PRT; 497 AA.
AC 043174;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME) (P450RAI) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26A1 OR CYP26.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97373542; PubMed=9228017;
RA White J.A., Beckett-Jones B., Guo Y.-D., Dilworth F.J., Bonasoro J.,
RA Jones G., Petkovich M.;
RT "cDNA cloning of human retinoic acid-metabolizing enzyme (hp450RAI)
RT identifies a novel family of cytochromes P450.";
RL J. Biol. Chem. 272:18538-18541(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98380037; PubMed=9716180;
RA Sonneveld E., van den Brink C.E., van der Leede B.M., Schulkes R.K.,
RA Petkovich M., van der Burg B., van der Saag P.T.;
RT "Human retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific for
RT all-trans-RA and can be induced through RA receptors in human breast
RT and colon carcinoma cells.";
RL Cell Growth Differ. 9:629-637(1998).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=99045433; PubMed=9826557;
RA Trofimova-Griffin M.E., Juchau M.R.;
RT "Expression of cytochrome P450RAI (CYP26) in human fetal hepatic and
```

```
RT cephalic tissues.";
RL Biochem. Biophys. Res. Commun. 252:487-491(1998).
CC -!- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEROISOMER 9-CIS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-
CC HYDROXYLATION. RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED
CC FORMS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: HIGHEST LEVELS IN ADULT LIVER, HEART,
CC PITUITARY GLAND, ADRENAL GLAND, PLACENTA AND REGIONS OF THE BRAIN.
CC -!- INDUCTION: BY RETINOIC ACIDS (RA).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005418; AAB88881.1; -.
DR MIM; 602239; -.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum.
FT BINDING 442 442 HEME (POTENTIAL).
SQ SEQUENCE 497 AA; 56162 MW; EAB6B84B24B2EAB3 CRC64;
```

Query Match 67.9%; Score 1741; DB 1; Length 497;
Best Local Similarity 68.2%; Pred. No. 3.8e-93;
Matches 339; Conservative 62; Mismatches 84; Indels 12; Gaps 5;

```
QY 1 MGLYTLMTVFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPFGTGLPFIGETLQL 60
Db 1 MGLPALLASALCTFVLPVLLFLAAIKLWLYCVSGDRSCALPLPPGTMGFFFGTGLQ 60
QY 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSQWPASVRTIL 120
Db 61 VLQRRKFLQMKRRKYGFIYKTHLFGNPTVRVMGADNVRILLGDDRLVSVHWPASVRTIL 120
QY 121 GSDTSLNVHGQHKKKKAIMRAFSRDALEHYIPVIOQEVKSAIQEWLQKDSCLVYPPEM 176
Db 121 GSGCLSNLHDSHKKQKVKVIMRAFSREALECYVPVITEVSGSLEQWL---SCGERGLY 177
QY 177 YPEMKKLMFRIAMRILLGFEPEQIKTD---EQELVEAFEMIKNLFSLPIDVPFSGLYRG 233
Db 178 YPEVKRLMFRIAMRILLGCEP-QLAGDGDSEQLVEAFEMTRNLFSLPIDVPFSGLYRG 236
QY 234 LRARFIHSKTEENIRKKIQD-DDNENQKQYKDALQLLIIENSRSDPEFSLQAMKEAATE 292
Db 237 MKARNLIHARIEQNIIRAKICGLRASEAGCGCKDALQLLIIHESWGERLDMQALKQSSTE 296
QY 293 LLFGGHETTASTATSLVMFLGLNTEVVQKRVREVEQKVEGMVTPGKGLSMELLQDKLYT 352
Db 297 LLFGGHETTASATSLITLYGLYPHVLQKRVREELSKGLCKSNQDNKLDMEILEQLKYI 356
QY 353 GCVIKETLRINPPVPGGFRVALKTEFELNGYQIPKGNVVIYSICDTHDVADVPFNKEEFQ 412
Db 357 GCVIKETLRINPPVPGGFRVALKTEFELNGYQIPKGNVVIYSICDTHDVAEIFTNKEEFNP 416
QY 413 ERFMSKGLDGSRFNYIPFGGGSRMCVKGKEFAKVLKIFLVELTQHNCNWLNSGPTMTKT 472
Db 417 DRFMLPHPEDASRFSFIPFGGGLRSCVKGKEFAKILLKIFTVELARHCDQNLNGPPTMKT 476
QY 473 GPTIYVVDNLPTKFTSY 489
Db 477 SPTVYVVDNLPAFETHF 493
```

```
RESULT 3
CP26_MOUSE
ID CP26_MOUSE STANDARD; PRT; 497 AA.
AC O55127;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING
DE CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE).
GN CYP26A1 OR CYP26 OR P450RA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RX MEDLINE=97392446; PubMed=9250660;
RA Fujii H., Sato T., Kaneko S., Gotoh O., Fujii-Kuriyama Y., Osawa K.,
RA Kato S., Hamada H.;
RT "Metabolic inactivation of retinoic acid by a novel P450
RT differentially expressed in developing mouse embryos.";
RL EMBO J. 16:4163-4173(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98113212; PubMed=9442090;
RA Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G.,
RA Metzger D., Chambon P., Petkovich M.;
RT "Mouse P450RA1 (CYP26) expression and retinoic acid-inducible retinoic
RT acid metabolism in F9 cells are regulated by retinoic acid receptor
RT gamma and retinoid X receptor alpha.";
RL J. Biol. Chem. 273:2409-2415(1998).
CC -!- FUNCTION: PLAYS A KEY ROLE IN RETINOIC ACID METABOLISM. ACTS ON
CC RETINOIDS, INCLUDING ALL-TRANS-RETINOIC ACID (RA) AND ITS
CC STEREOISOMER 9-CIS-RA. CAPABLE OF BOTH 4-HYDROXYLATION AND 18-
CC HYDROXYLATION. RESPONSIBLE FOR GENERATION OF SEVERAL HYDROXYLATED
CC FORMS OF RA, INCLUDING 4-OH-RA, 4-OXO-RA, AND 18-OH-RA.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RETINOIC ACIDS (RA).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y12657; CAA73206.1; -.
DR MGD; MGI:1096359; Cyp26.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum.
FT BINDING 442 442 HEME (POTENTIAL).
SQ SEQUENCE 497 AA; 56177 MW; 33B07D7C29134471 CRC64;
Query Match 67.7%; Score 1734; DB 1; Length 497;
Best Local Similarity 67.7%; Pred. No. 9.7e-93;
Matches 336; Conservative 61; Mismatches 89; Indels 10; Gaps 4;
QY 1 MGLYTLMTVFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPTGMLPFIGETLQL 60
||| | : ||| ||| : ||| : : | : ||| ||| ||| ||| :
Db 1 MGLPALLASALCTFVLPVLLFLAALKLWDLYCVSSRRDSCALPLPPTGTMGFPFFGETLQM 60
QY 61 ILQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRRQILLGEHKLVSQVWPASVRTL 120
: ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 VLQRRKFLQMKRRKYGFIYKTHLFGNPTVRVMGADNVRRILLGEHRLVSVHWPASVRTL 120
```

```
QY 121 GSDTLSNVHGVOHKKKKAIRAFSRDALEHYIPVQQEVKSAIQEWLQKDS-----VLV 176
| : ||| : | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 121 GAGCLSNLHDSHKQKKVIMQAFSRALOCYVLVIAEVSCLQWL---SCGERGLV 177

QY 177 YPEMKKLMFRIAMRILLGEPEQI--KTDEQELVEAFEEMIKNLSLPIDVPFSGLYRGL 234
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 178 YPEVKRLMFRIAMRILLGCEPGPAGGEDEQQLVEAFEEMIRNLSLPIDVPFSGLYRGV 237

QY 235 RARNFHSKIEENIRKKIQD-DDNENQKYKDALQLLIENSRSDPEPFSLOAMKEATEL 293
: ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 238 KARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWGERLDMQALKQSSTEL 297

QY 294 LFGGHETTASTATSLVMFLGLNTEVVQKRVREYQKVMGYTPGKGLSMELLQKLYTG 353
||| ||| ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 298 LFGGHETTASAATSLITYLGLYPHVLOKVRREIKSKGLCKSNQDNKLDMETLEQLKYIG 357

QY 354 CVIKETLRINPPVGGFRVALKTFELNGYQIPKGNVIYSICDTHDVAADVFPNKEEFOPE 413
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| : |||
Db 358 CVIKETLRINPPVGGFRVALKTFELNGYQIPKGNVIYSICDTHDVAADVFPNKEEFPD 417

QY 414 REMSKGLEDSRFNYPFGGSRMVCVGEFAKVILKIFLVELTQHCNWLISNGPPTMKTG 473
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 418 RFIVPHPEDASRFSFIPFGGLRSCVGEFAKILKIFTVELARHCDWQLNGPPTMKTIS 477

QY 474 PTIYPVDNLPTKFTSY 489
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 478 PTIYPVDNLPTKFTSY 493

RESULT 4
C901_ARATH
ID C901_ARATH STANDARD; PRT; 472 AA.
AC Q42569;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 90A1 (EC 1.14.-.-).
GN CYP90A1 OR CYP90 OR CPD.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=96200769; PubMed=8612270;
RA Szekeres M., Nemeth K., Koncz-Kalman Z., Mathur J., Kauschmann A.,
RA Altmann T., Redei G.P., Nagy F., Schell J., Koncz C.;
RT "Brassinosteroids rescue the deficiency of CYP90, a cytochrome P450,
RT controlling cell elongation and de-etiolation in Arabidopsis.";
RL Cell 85:171-182(1996).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X87367; CAA60793.1; -.
DR EMBL; X87368; CAA60794.1; -.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; p450; 2.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Heme.
FT BINDING 418 418 HEME (BY SIMILARITY).
SQ SEQUENCE 472 AA; 53785 MW; 41A73F46D64E343F CRC64;
```


SQ SEQUENCE 518 AA; 59210 MW; 9B93AA12E617D0DF CRC64;

Query Match 13.7%; Score 350.5; DB 1; Length 518;
Best Local Similarity 25.6%; Pred. No. 2e-13;
Matches 112; Conservative 83; Mismatches 206; Indels 37; Gaps 10;

QY 46 PGTMLPFIGETLQILQRRKQYKGYKTHLFGNPTVRVMGADNVRQILGE- 104
|| ||| : | : | ||| : : | ||| : : | : : : | :
Db 40 PGPKPLPYEGTMLEYKKGFTNDETCFQYGRIGYIDGRQVLCIMDKSMIKTVLKEC 99

QY 105 HKLVSVQWPASVRTILGSDTSLSNVHGQVHKMKKAIMRAFSRDALEHYIPVIOQE--VK 161
: : : : | | | : : : : : : : : : : : : : :
Db 100 YNIFTNRRNFHLNGEL-FDALSVAEDDTWRIRSVLSPSFTSGRLKEMFGIMQHSSTLL 158

QY 162 SAIQEWLQKDSCLVYPKMLFMRIAMRIL---LGEPEQIKTDEQELVEAFEEMIK- 216
| : : : | : : : | : : : | : : : | : : : | : : :
Db 159 SGMKKQADKDQTI---EVKEFGPYSDVVTSTAFSDVSDISLNPSPDFVSNVKKMLKF 214

QY 217 ---NLFSLPIDVPESGLYRGLRARNFIHSEKIEE---NIRKKIODDDNENEQYKDALQ 268
||| ||| : | : | : | : | : | : | : | : | : | :
Db 215 DLNPLFLVLALEPFTGPILKMKFSFFPAVDTDFYASLAKIKSGRDTGNSTNRVDFLQ 274

QY 269 LLIENSRSDPEFSLQAMK-----EATELLFGGHETTASTATSLVMFLGINTVVQ 320
| : : : | : : : | : : : | : : : | : : : | : : :
Db 275 LMTDSQSGDTKTGEQTKGLTDEHILSQAMIFIFAGVETSSSTMSFLAYLNATNHHVMT 334

QY 321 KYREEVQKXVEMGMYPGKG-LSMELLDQLKYTCVIKETLRINPPVPGGFRVAKITFEL 379
| : : : | : : : | : : : | : : : | : : : | : : :
Db 335 KLQEEID-----TVFPNKAPIQYEALMQMDYLDCLVNESRLYPIAPRLRERVAKTVEI 388

QY 380 NGYQIPKGNVVIYSICDTHDVADVPNKKEEPQPERFMSKGLDGSRFNYPFGGSRMCV 439
|| ||| | : : : | : : : | : : : | : : : | : : :
Db 389 NGIVIPKDCIVLVPTWTLHRDPEIWSDPDEPKPERFSKENKESIDPYTYMPFGAGPRNCI 448

QY 440 KKEFAKVLKIFLVELTQ 457
| | : : : | : : : | : : : | : : : | : : :
Db 449 GMRFALIMIKLAMVELLQ 466

RESULT 10
CP36_RABIT STANDARD; PRT; 501 AA.
ID CP36_RABIT STANDARD; PRT; 501 AA.
AC P11707; Q29506;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 3A6 (EC 1.14.14.1) (CYP11A6) (P450-3C).
GN CYP3A6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166352; PubMed=3349903;
RA Dalet C., Clair P., Daujat M., Fort P., Blanchard J.-M., Maurel P.;
RT "Complete sequence of cytochrome P450 3c cDNA and presence of two
RT mRNA species with 3' untranslated regions of different lengths";
RL DNA 7:39-46(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89380226; PubMed=2777787;
RA Potenza C.L., Pendurthi U.R., Strom D.K., Tukey R.H., Griffin K.J.,
RA Schwab G.E., Johnson E.F.;
RT "Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent
RT expression and transcriptional activation by rifampicin";
RL J. Biol. Chem. 264:16222-16228(1989).
CC -!- FUNCTION: EXHIBITS PROGESTERONE 6 BETA-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RIFAMPICIN.

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M19139; AAA31430.1; -.
DR EMBL; J05034; AAA31178.1; -.
DR PIR; A29487; A29487.
DR InterPro; IPR001128; -.
DR InterPro; IPR002397; -.
DR InterPro; IPR002401; -.
DR InterPro; IPR002402; -.
DR InterPro; IPR002403; -.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00359; BP450.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00463; BP450I.
DR PRINTS; PR00464; BP450II.
DR PRINTS; PR00465; BP450IV.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 440 440 HEME (BY SIMILARITY).
FT CONFLICT 54 55 GI -> VIN (IN REF. 1).
FT CONFLICT 165 169 GKPVD -> ASPST (IN REF. 1).
FT CONFLICT 393 393 MISSING (IN REF. 1).
FT CONFLICT 494 495 RD -> ES (IN REF. 1).
SQ SEQUENCE 501 AA; 57450 MW; 251D21061863ACFB CRC64;

Query Match 13.4%; Score 343.5; DB 1; Length 501;
Best Local Similarity 26.8%; Pred. No. 4.9e-13;
Matches 126; Conservative 88; Mismatches 163; Indels 93; Gaps 19;

QY 46 PGTMLPFIGETLQILQRRK----FLMKRQKYGCIYKTHLFGNPTVRVMGADNVRQIL 101
|| ||| ||| : | : | ||| : : | ||| : : | : : : | :
Db 37 PGPTPLPFIG----TILEYRKGIWDFIECRKKYGNMGLFDGRQPLMVTDPDMIKTVL 92

QY 102 LGE-----HKLVSV---QWPASVRTILGSDTSLSNVHGQVHKMKKRAI 140
: | : | : | : | : | : | : | : | : | : | : | :
Db 93 VKECYSVETNRRSEFGPVGFMKKAVIDEDW-KRVKTLSP----- 133

QY 141 MRAFSRDALEHYIPVIOQE----VKSIAQEWLQKDSCLVYPKMLFMRIAMRIL---- 192
| : : : | : : : | : : : | : : : | : : : | : : :
Db 134 --TFTSGKLKEMFLIAQYGDVLVKNLRQE-AEKGPV---DLKEIFGAYSMDVITGS 186

QY 193 LGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDV-----PF-SGLYRGLR-----ARNF 239
| : : : | : : : | : : : | : : : | : : : | : : :
Db 187 FGVNIDSLRNPQDPFVKNVRRLKFSFDFDPLLSITLFPFLTPIFEALHISMFPKDVMD 246

QY 240 IHSKIEENIRKKIODDDNENEQYK-DALQLLI--ENSRSDPEFSLQAMKEAATE--LL 294
: : : | : : : | : : : | : : : | : : : | : : :
Db 247 LKTSVE----KIKDRLKDKQKRRVDFLQLMINSQSKIDS HKALDDIEVVAQSIIL 301

QY 295 FGGHETTASTATSLVMFLGINTVEVQKVEEVQEKVEMGMYPGKGL-SMELLDQLKYTG 353
| : : : | : : : | : : : | : : : | : : : | : : :
Db 302 FAGYETTSSTLSFIMHLLATHPDVQKQKLOEIDTLL-----PNKELATYDTLVKMEYLD 355

QY 354 CVIKETLRINPPVPGGFRVAKLTFELNGYQIPKGNVVIYSICDTHDVADVPNKKEEFOPE 413
| : : : | : : : | : : : | : : : | : : : | : : :
Db 356 MVVNETLRLYPIAGRLERVCKKDVDTINGTIPKGTIVMPTYALHRDPQHWTEPDEFRDE 415

QY 414 RFMSKGLDGSRFNYPFGGSRMCVKGFAKVLKIFLVELTQHCNWIL 463
|| : : : | : : : | : : : | : : : | : : : | : : :
Db 416 RFSKKNKDINPIYHPFGAGPRNCLGMRFAIMNLIKALVRLMQNFSKL 465

RESULT 11

```

CPC9_HUMAN
ID CPC9_HUMAN STANDARD; PRT; 490 AA.
AC P11712;
DT 01-OCT-1989 (Rel. 12, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME P450 2C9 (EC 1.14.14.1) (CYP11C9) (P450 PB-1) (P450 MP-4)
DE (S-MEPHENYTOIN 4-HYDROXYLASE) (P-450MP).
GN CYP2C9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88103561; PubMed=2827463;
RA Meehan R.R., Gosden J.R., Rout D., Hastie N.D., Friedberg T.,
RA Adesnik M., Buckland R., van Heyningen V., Fletcher J., Spurr N.K.,
RA Sweeney J., Wolf C.R.;
RT "Human cytochrome P-450 PB-1: a multigene family involved in
RT mephenytoin and steroid oxidations that maps to chromosome 10.";
RL Am. J. Hum. Genet. 42:26-37(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88096500; PubMed=3697070;
RA Kimura S., Pastewka J., Gelboin H.V., Gonzalez F.J.;
RT "cDNA and amino acid sequences of two members of the human P450IIC
RT gene subfamily.";
RL Nucleic Acids Res. 15:10053-10054(1987).
RN [3]
RP SEQUENCE OF 108-490 FROM N.A.
RX MEDLINE=89062423; PubMed=3196692;
RA Ged C., Umbenhauer D.R., Bellow T.M., Bork R.W., Srivastava P.K.,
RA Shinriki N., Lloyd R.S., Guengerich F.P.;
RT "Characterization of cDNAs, mRNAs, and proteins related to human
RT liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase.";
RL Biochemistry 27:6929-6940(1988).
RN [4]
RP VARIANTS.
RX MEDLINE=97101957; PubMed=8946475;
RA Stubbins M.J., Harries L.W., Smith G., Tarbit M.H., Wolf C.R.;
RT "Genetic analysis of the human cytochrome P450 CYP2C9 locus.";
RL Pharmacogenetics 6:429-439(1996).
RN [5]
RP VARIANTS.
RX MEDLINE=97264536; PubMed=9110362;
RA Bhasker C.R., Miners J.O., Coulter S., Birkett D.J.;
RT "Allelic and functional variability of cytochrome P4502C9.";
RL Pharmacogenetics 7:51-58(1997).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: BY RIFAMPIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -!- DATABASE: NAME=Cytochrome P450 Allele Nomenclature Committee;
CC NOTE=CYP2C9 alleles;
CC WWW="http://www.imm.ki.se/cypalleles/cyp2c9.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M21940; AAA52159.1; -.
DR PIR; A28530; A28530

```



```
ID CPCA_HUMAN STANDARD; PRT; 490 AA.
AC P11713;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 2C10 (EC 1.14.14.1) (CYP11C10) (P450 MP-8) (S-
DE MEPHENYTOIN 4-HYDROXYLASE) (P-450MP).
GN CYP2C10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 6-490 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=87185403; PubMed=3032244;
RA Umbenhauer D.R., Martin M.V., Lloyd R.S., Guengerich F.P.;
RT "Cloning and sequence determination of a complementary DNA related to
RT human liver microsomal cytochrome P-450 (S)-mephenytoin 4-hydroxylase.";
RL Biochemistry 26:1094-1099(1987).
RN [2]
RP SEQUENCE OF 6-490 FROM N.A.
RX MEDLINE=89062423; PubMed=3196692;
RA Ged C., Umbenhauer D.R., Bellew T.M., Bork R.W., Srivastava P.K.,
RA Shinriki N., Lloyd R.S., Guengerich F.P.;
RT "Characterization of cDNAs, mRNAs, and proteins related to human
RT liver microsomal cytochrome P-450 (S)-mephenytoin 4'-hydroxylase.";
RL Biochemistry 27:6929-6940(1988).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
CC TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
CC AND CARCINOGENS.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15331; AAA52157.1; -.
DR EMBL; M21939; AAA52158.1; -.
DR PIR; A27541; A27541.
DR PIR; D28951; D28951.
DR MTM; 124020; -.
DR InterPro; IPR001128; -.
DR InterPro; IPR002401; -.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00463; EP450I.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 435 435 HEME (BY SIMILARITY).
SQ SEQUENCE 490 AA; 55625 MW; 4FDC13A83AE494DE CRC64;

Query Match 13.2%; Score 339.5; DB 1; Length 490;
Best Local Similarity 26.9%; Pred. No. 8.1e-13;
Matches 139; Conservative 83; Mismatches 218; Indels 77; Gaps 22;

QY 5 TLMVTFICTVLPVLLFLAAVKLWMLTIRVDNCRSPLPPTGMLPFGTETLQL-ILQ 63
:|:| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 SLVVLVLC---LSCLLLS---LWR-----QSGRGKLPPTPLPVIGNILQIGIKD 49
```

```
QY 64 RRKFLRMKQKYGCIYKTHLFGNPTVRVMGADNVRQL--LGEHKLVSQVWPASVRTILG 121
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 50 ISKSLTNLSKVYGPVFTLYFGLKPIVVLHGYEAVKEALIDLGEFSGRGIFPLAERANG 109
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 122 SDTSLNVHGVQHKKKK-AIMRAFSRDALHYIPVQQEVKSAIQEWLQKDCSVLYPEM 180
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 110 -----FGIVFSNGKKWKEIRRESLMTLRF-----GMGKRSTEDRVQEEARCLVEELR 157
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 181 KKLMEFIAMRILLGFEPEQI-----KTDEQ--ELVEAFEEMIK-----N 217
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 158 KTKASPCDPTFILGCAPCNVICSIIIFHKRFDYKQQQFLNLMKENIKILSSPWIQICN 217
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 218 LFSLPIDVPFSGLYRGLRARN--FIHSKIEENIRKKIQDDDDNENEQYKDALQLLIENS 275
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 218 NFSPIIDY-FPGTHNKL-LKNVAFMKSYILEKVKHQESMDMNPQDFIDCLMKMEKEK 275
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 276 RSD-EFPSLQAMKEATELLFGGHETTASTATSLVPLGLNTEVVQKRVREEVQEKVEMGM 334
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 276 HNQPSEFTIESLENTAVDLFGAGTETTTSTLRYALLLLKHPVTAQVQEEIERVI---- 331
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 335 YTPGKGLS--MELLDQLKYTGCVIKETLRINPPVPGGFRVALK-TFELNGYQIPKGNVVI 391
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 332 ---GRNRSPCMQDRSHMPYTDVAVVHEVQRCIDLLPTSLPHAVTCDIKFRNYLIPKGTTL 388
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 392 YSICDT-HDVADVFPNKEEFQPERFMSKGLDGSRFN----YIPFGGGRMCVQKEFAKV 446
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 389 ISLTSVLHDNKE-FNPMEFDPHF-----LDEGDNFKSKYFMPFSGAGKRICVGEALAGM 443
| | : | | : | | : | | : | | : | | : | | : | | : | |
QY 447 LLKIFVELTQHCNWLISNGPPTMKTGTTIYPVDNLP 483
| | : | | : | | : | | : | | : | | : | | : | | : | |
Db 444 ELFLFTLSLQNFENLKSVDPKNLDITPVVNGFASVP 480
| | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 13
CP39_RAT STANDARD; PRT; 503 AA.
ID CP39_RAT
AC P51538; Q64631; Q64557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 3A9 (EC 1.14.14.1) (CYP11A9) (P450-OLF3) (OLFACTIVE)
DE (3AH15).
GN CYP3A9.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=97144501; PubMed=8990268;
RA Mahnke A., Strotkamp D., Roos P.H., Hanstein W.G., Chabot G.G.,
RA Nef P.;
RT "Expression and inducibility of cytochrome P450 3A9 (CYP3A9) and
RT other members of the CYP3A subfamily in rat liver.";
RL Arch. Biochem. Biophys. 337:62-68(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96220175; PubMed=8660328;
RA Wang H., Kawashima H., Strobel H.W.;
RT "cDNA cloning of a novel CYP3A from rat brain.";
RL Biochem. Biophys. Res. Commun. 221:157-162(1996).
CC -!- FUNCTION: THIS ISOZYME SEEMS TO BE IMPLICATED IN OLFACTION. ACTIVE
CC IN THE DEMETHYLATION OF ERYTHROMYCIN AS WELL AS BENZPHETAMINE.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN OLFACTORY EPITHELIUM.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration.
```



```
DR FlyBase; FBgn0015033; Cyp4d8.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
KW Endoplasmic reticulum.
FT BINDING 451 451 HEME (BY SIMILARITY).
FT CONFLICT 333 333 A -> E (IN REF. 2).
FT CONFLICT 435 435 R -> C (IN REF. 2).
SQ SEQUENCE 505 AA; 57819 MW; 7BAA5271ED46093F CRC64;

Query Match 12.9%; Score 331; DB 1; Length 505;
Best Local Similarity 26.4%; Pred. No. 2.6e-12;
Matches 129; Conservative 82; Mismatches 211; Indels 66; Gaps 17;

QY 18 VLLFLAAVKL-----WELMIRRVDPNCRSLPPGFMGLPFIGE-TLQLILQRRKFLRMKR 72
Db :||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 73 Q---KGCYKTHLFGNPTVVRMGADNVRQILLGEHKLV-----VQMPASVRTILGS 122
Db : | | | : : : | | : | | : | | : | | : | | : | | : | | : | | :
QY 60 EYVLKFGHLQRVWIFNRLIMSGDAELNEQLSSQEHVKKHPYKVLGQW-----LGN 112
Db : | | | : : : | | : | | : | | : | | : | | : | | : | | : | | :
QY 123 DTLSNVHGVOHKKKKAIMRAFSDALEHYIPVQEVKSAIQEWLQK--DSCVLVYDEM 180
Db : | | : : | | | | | | | | | | | | | | | | | | | | | | : | | :
QY 113 GLLSDGKVWHQ-RRKIITPTFHFSILEQFVEVFDQSQNICVQRLAKANGTFDVYRSI 171
QY 181 KKLFRIAMRILLGFEPEQIKTDEQELVEAFEEIMKNL-----FSLPIDVFPFSGLYRGL 234
Db : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 172 CAAALDIAETAMGTKIYAQANESTPYAEAVNECTALLSWRFMSVYLQVELLTLTHPHL 231
QY 235 RAR--NFIHS-----KIEENIRKKIQDD-----DNENEQYKDALQLLIENSRRSD 278
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 232 KWRQTQLRTMQEFTIKVIEKRRQALEDDQSKLMDTADVDGSKRRMALLDVLMLSTVDG 291
QY 279 EPFSLQAMKEAATELFGGHETTASTATSLVMFLGLNTEWQKVREEVQEKVEMGYTPG 338
Db : : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 292 RPLTNDIEEREVDTFMFEHDTTTSALSFCLHLSRHPVEVQAKMLEEIVQVLGDRSRP- 350
QY 339 KGLSMELLDLQKYTGCVIKETLRINPPVPGGFRVALKTFEL-----NGYQIPKGNVVIY 392
Db : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 351 --VSIRDLGELKYMCEVIKESLRMPPVPIVGRKLQTDKETHSVHGDGV-IPAGSEIII 407
QY 393 SICDTHDVADVFPNKEEFQPERFMSKGLDGSR---FNVIPFGGSRMCVCGKEFAKVLK 449
Db : | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 408 GIFGVHRQETFPNPDEFLPERH-----ENGSRVAPFKMIPFSAFPRNCIGQKFAQLEMK 462
QY 450 IFVELTQ 457
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 463 MMLAKIVR 470

RESULT 15
CPXN_ANASP
ID CPXN_ANASP STANDARD; PRT; 459 AA.
AC P29980; Q59131;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROBABLE CYTOCHROME P450 110 (EC 1.14.-.-) (ORF3).
GN CYP110.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072249; PubMed=2123860;
RA Lammers P.J., McLaughlin S., Papin S., Trujillo-Provencio C.,
RA Ryncarz A.J. II;
RT "Developmental rearrangement of cyanobacterial nif genes: nucleotide
sequence, open reading frames, and cytochrome P-450 homology of the
```

```
RT Anabaena sp. strain PCC 7120 nifd element.";
RL J. Bacteriol. 172:6981-6990(1990).
RN [2]
RP REVISIONS.
RA Lammers P.J., Trujillo-Provencio C., Sanchez C., Carillo M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN ALKANE/FATTY ACID HYDROXYLASE.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U38537; AAC82967.1; -.
DR PIR; C37842; C37842.
DR InterPro; IPR001128; -.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Oxidoreductase; Monooxygenase; Electron transport; Heme;
KW Nitrogen fixation.
FT BINDING 393 393 HEME (BY SIMILARITY).
SQ SEQUENCE 459 AA; 52525 MW; 67C62908C94C5698 CRC64;

Query Match 12.9%; Score 330.5; DB 1; Length 459;
Best Local Similarity 25.3%; Pred. No. 2.5e-12;
Matches 114; Conservative 88; Mismatches 211; Indels 37; Gaps 14;

QY 46 PGTMLPFIGETLQLLQRRKFLMRKQKGYCIYKTHLFGNPTVVRMGADNVRQILLGEH 105
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 6 PNPISVPSWQLINWIADPIGFQKKYKKNIFSMQLAGISFVILGEPQALQEITQD 65
Db : : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 106 KLVSV-QWPASVETILGSDTLNVHGQHKKKKAIMRAFSDALEHYIPVQEVKSAI 164
Db : : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 66 SRFDVGRGNTLAEPLIGRTSLMLMDGDRRRERKLLMPPFHGERLQAYAQICLITNQIA 125
QY 165 QEWLQKDSCLVYPPEMKKLMERIAMRILLGFEP----EQIK---TDEQELVEA-FEEMIK 216
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 126 SEW-QIGQPFVARSAMQKLSLEVIIQIVFGLADGERYQQIKPLETDWLNMTDSPLRSSML 184
QY 217 NLFSLPID---VFPFSGLYRGLRA-RNFTHSKIEENIRKKIQDDNENEQYKDALQLLI 271
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 185 FLKSLQKDWGTWIPWQMKHKQRSIYDLLOAEIEEKTK-----ENEQR-GDVLSLMM 236
QY 272 ENSRRSDEPFSLQAMKEAATELFGGHETTASTATSLVMFLGLNTEVQKVREEVQEKVE 331
Db : : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 237 AARDENGQAMTDEELKDELLTILFAGHETTATTIAWAFY-----QILKNV--NVQEKLQ 288
QY 332 MGMTYTPGKGLSMELLDLQKYTGCVIKETLRINPPVPGGF-RVALKTFELNGYQIPKGNV 390
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 289 QELDRIGANPNPMEIAQLPYLTAVSQETLRMVPVLPVLTLPRIKTSINIAGYQLEPDTTL 348
QY 391 IYSICDTHDVADVFPNKEEFQPERFMSKGLDGSRFNVIPFGGSRMCVCGKEFAKVLKI 450
Db : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 349 MASIYLIHYREDLYPNPQQFRPERFIER---QYSPSEYIPFGGSRRCGLGIALALLEIKL 405
QY 451 FLVELTQHCNWLNSGPP--TMKTGPTIYP 478
Db : : : | | : | | : | | : | | : | | : | | : | | : | | : | | :
QY 406 VIATVLSNYQLALAEDKPVNVQRRGFTLAP 435

Search completed: November 6, 2001, 13:39:39
Job time: 242 sec
```

